

# SEQUENCE LISTING

<110> Flodgaard, Hans Jakob  
Lindbom, Lennart  
Bjoern, Soeren

<120> Inhibition Of Bradykinin Release

<130> 5694.200-US

<150> 60/132,748

<151> 1999-04-29

<150> 60/157,384

<151> 1999-10-01

<160> 14

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 225

<212> PRT

<213> Homo sapiens

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Ala	Arg	Phe	Val	Met	Thr	Ala	Ala	Ser	Cys	Phe	Gln	Ser	Gln	Asn	Pro
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Gly	Val	Ser	Thr	Val	Val	Leu	Gly	Ala	Tyr	Asp	Leu	Arg	Arg	Arg	Glu
	50					55					60				
Arg	Gln	Ser	Arg	Gln	Thr	Phe	Ser	Ile	Ser	Ser	Met	Ser	Glu	Asn	Gly
65				70						75				80	
Tyr	Asp	Pro	Gln	Gln	Asn	Leu	Asn	Asp	Leu	Met	Leu	Leu	Gln	Leu	Asp
				85				90					95		
Arg	Glu	Ala	Asn	Leu	Thr	Ser	Ser	Val	Thr	Ile	Leu	Pro	Leu	Pro	Leu
			100					105					110		
Gln	Asn	Ala	Thr	Val	Glu	Ala	Gly	Thr	Arg	Cys	Gln	Val	Ala	Gly	Trp
		115					120				125				
Gly	Ser	Gln	Arg	Ser	Gly	Gly	Arg	Leu	Ser	Arg	Phe	Pro	Arg	Phe	Val
	130				135						140				
Asn	Val	Thr	Val	Thr	Pro	Glu	Asp	Gln	Cys	Arg	Pro	Asn	Asn	Val	Cys
145					150				155					160	
Thr	Gly	Val	Leu	Thr	Arg	Arg	Gly	Gly	Ile	Cys	Asn	Gly	Asp	Gly	Gly
			165					170					175		
Thr	Pro	Leu	Val	Cys	Glu	Gly	Leu	Ala	His	Gly	Val	Ala	Ser	Phe	Ser
			180				185						190		
Leu	Gly	Pro	Cys	Gly	Arg	Gly	Pro	Asp	Phe	Phe	Thr	Arg	Val	Ala	Leu
		195					200					205			
Phe	Arg	Asp	Trp	Ile	Asp	Gly	Val	Leu	Asn	Asn	Pro	Gly	Pro	Gly	Pro
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Ala															
225															

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<211> 678

<212> DNA  
<213> Homo sapiens

<400> 2

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agctgcttcc	aaagccagaa	ccccgggggt	agcaccgtgg	tgctgggtgc	ctatgacctg	180
agggcgccgg	agaggcagtc	ccgccagacg	ttttccatca	gcagcatgag	cgagaatggc	240
tacgaccccc	agcagaacct	gaacgacctg	atgctgcttc	agctggaccg	tgaggccaac	300
ctcaccagca	gcgtgacgat	actgccactg	cctctgcaga	acgccacggg	ggaagccggc	360
accagatgcc	aggtggccgg	ctggggggagc	cagcgcagtg	gggggcgtct	ctcccgtttt	420
cccaggttcg	tcaacgtgac	tgtgaccccc	gaggaccagt	gtcgcccaaa	caacgtgtgc	480
accggtgtgc	tcacccgccg	cggtggccatc	tgcaatgggg	acggggggcac	ccccctcgtc	540
tgcgagggcc	tggcccacgg	cgtggccctcc	ttttccctgg	ggccctgtgg	ccgaggccct	600
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ggaccggggc	cagcctag					678

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<213> Homo sapiens

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gcttcgtgat	gaccgcggcc	agctgcttcc	aaagccagaa	ccccgggggt	agcaccgtgg	180
tgctgggtgc	ctatgacctg	agggcgccgg	agaggcagtc	ccgccagacg	ttttccatca	240
gcagcatgag	cgagaatggc	tacgaccccc	agcagaacct	gaacgacctg	atgctgcttc	300
agctggaccg	tgaggccaac	ctcaccagca	gcgtgacgat	actgccactg	cctctgcaga	360
acgccacggg	ggaagccggc	accagatgcc	aggtggccgg	ctggggggagc	cagcgcagtg	420
gggggcgtct	ctcccgtttt	cccaggttcg	tcaacgtgac	tgtgaccccc	gaggaccagt	480
gtcgcccaaa	caacgtgtgc	accggtgtgc	tcacccgccg	cggtggccatc	tgcaatgggg	540
acggggggcac	ccccctcgtc	tgcgagggcc	tggcccacgg	cgtggccctcc	ttttccctgg	600
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<213> Homo sapiens

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			20					25				30			
Cys	Gly	Gly	Ala	Leu	Ile	His	Ala	Arg	Phe	Val	Met	Thr	Ala	Ala	Ser
			35				40				45				
Cys	Phe	Gln	Ser	Gln	Asn	Pro	Gly	Val	Ser	Thr	Val	Val	Leu	Gly	Ala
			50			55					60				
Tyr	Asp	Leu	Arg	Arg	Arg	Glu	Arg	Gln	Ser	Arg	Gln	Thr	Phe	Ser	Ile
65					70				75					80	
Ser	Ser	Met	Ser	Glu	Asn	Gly	Tyr	Asp	Pro	Gln	Gln	Asn	Leu	Asn	Asp
				85				90						95	
Leu	Met	Leu	Leu	Gln	Leu	Asp	Arg	Glu	Ala	Asn	Leu	Thr	Ser	Ser	Val
				100				105					110		
Thr	Ile	Leu	Pro	Leu	Pro	Leu	Gln	Asn	Ala	Thr	Val	Glu	Ala	Gly	Thr
				115			120					125			
Arg	Cys	Gln	Val	Ala	Gly	Trp	Gly	Ser	Gln	Arg	Ser	Gly	Gly	Arg	Leu
				130		135					140				
Ser	Arg	Phe	Pro	Arg	Phe	Val	Asn	Val	Thr	Val	Thr	Pro	Glu	Asp	Gln
145					150				155					160	

Cys Arg Pro Asn Asn Val Cys Thr Gly Val Leu Thr Arg Arg Gly Gly  
 165 170 175  
 Ile Cys Asn Gly Asp Gly Gly Thr Pro Leu Val Cys Glu Gly Leu Ala  
 180 185 190  
 His Gly Val Ala Ser Phe Ser Leu Gly Pro Cys Gly Arg Gly Pro Asp  
 195 200 205  
 Phe Phe Thr Arg Val Ala Leu Phe Arg Asp Trp Ile Asp Gly Val Leu  
 210 215 220  
 Asn Asn Pro Gly Pro Gly Pro Ala  
 225 230

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 <212> DNA  
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 ctggcctcca ttcagaatca aggcaggcac ttctgcgggg gtgccctgat ccatgccgcg 180  
 ttctgtgatga ccgcggccag ctgcttccaa agccagaacc ccgggggttag caccgtgggtg 240  
 ctgggtgcct atgacctgag gcggcgggag aggcagtccc gccagacgtt ttccatcagc 300  
 agcatgagcg agaattggcta cgacccccag cagaacctga acgacctgat gctgcttcag 360  
 ctggaccgtg aggccaaacct caccagcagc gtgacgatac tgccactgcc tctgcagaac 420  
 gccacgggtg aagccggcac cagatgccag gtggccggct gggggagcca gcgcagtggg 480  
 gggcgctctc ccggttttcc caggttcgtc aacgtgactg tgacccccga ggaccagtgt 540  
 cgcccccaaca acgtgtgcac cgggtgtgctc acccgccgcg gtggcatctg caatggggac 600  
 gggggcaccc cctcgtctc cgagggcctg gccacggcg tggcctcctt ttccctgggg 660  
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 Ser Arg Ala Gly Ser Ser Pro Leu Leu Asp Ile Val Gly Gly Arg Lys  
 20 25 30  
 Ala Arg Pro Arg Gln Phe Pro Phe Leu Ala Ser Ile Gln Asn Gln Gly  
 35 40 45  
 Arg His Phe Cys Gly Gly Ala Leu Ile His Ala Arg Phe Val Met Thr  
 50 55 60  
 Ala Ala Ser Cys Phe Gln Ser Gln Asn Pro Gly Val Ser Thr Val Val  
 65 70 75 80  
 Leu Gly Ala Tyr Asp Leu Arg Arg Arg Glu Arg Gln Ser Arg Gln Thr  
 85 90 95  
 Phe Ser Ile Ser Ser Met Ser Glu Asn Gly Tyr Asp Pro Gln Gln Asn  
 100 105 110  
 Leu Asn Asp Leu Met Leu Leu Gln Leu Asp Arg Glu Ala Asn Leu Thr  
 115 120 125  
 Ser Ser Val Thr Ile Leu Pro Leu Pro Leu Gln Asn Ala Thr Val Glu  
 130 135 140  
 Ala Gly Thr Arg Cys Gln Val Ala Gly Trp Gly Ser Gln Arg Ser Gly  
 145 150 155 160  
 Gly Arg Leu Ser Arg Phe Pro Arg Phe Val Asn Val Thr Val Thr Pro  
 165 170 175  
 Glu Asp Gln Cys Arg Pro Asn Asn Val Cys Thr Gly Val Leu Thr Arg  
 180 185 190  
 Arg Gly Gly Ile Cys Asn Gly Asp Gly Gly Thr Pro Leu Val Cys Glu

195                      200                      205  
 Gly Leu Ala His Gly Val Ala Ser Phe Ser Leu Gly Pro Cys Gly Arg  
     210                      215                      220  
 Gly Pro Asp Phe Phe Thr Arg Val Ala Leu Phe Arg Asp Trp Ile Asp  
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 Gly Lys His

<210> 8  
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